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R.D.L.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/489,850

DATE: 08/08/2001
TIME: 16:14:04

Input Set : N:\Crf3\RULE60\09489850.txt
Output Set: N:\CRF3\08082001\I489850.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: VAN ALSTYNE, Diane

7 SHARMA, Lawrence Rajendra

9 (ii) TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPE SITES FOR
10 BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
11 CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF

13 (iii) NUMBER OF SEQUENCES: 75

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Foley & Lardner

17 (B) STREET: 3000 K Street, N.W., Suite 500

18 (C) CITY: Washington

19 (D) STATE: D.C.

20 (E) COUNTRY: USA

21 (F) ZIP: 20007-5109

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US/09/489,850

C--> 31 (B) FILING DATE: 24-Jan-2000

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/988,444

36 (B) FILING DATE:

38 (A) APPLICATION NUMBER: US 08/127,499

39 (B) FILING DATE: 28-SEP-1993

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: BENT, Stephen A.

43 (B) REGISTRATION NUMBER: 29,768

44 (C) REFERENCE/DOCKET NUMBER: 51916/103/INBI

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: (202)672-5300

48 (B) TELEFAX: (202)672-5399

49 (C) TELEX: 904136

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 992 amino acids

56 (B) TYPE: amino acid

57 (C) STRANDEDNESS:

58 (D) TOPOLOGY: unknown

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

66 Met Ala Ser Thr Thr Pro Ile Thr Met Glu Asp Leu Gln Lys Ala Leu

67 1 5 10 15

69 Glu Ala Gln Ser Arg Ala Leu Arg Ala Gly Leu Ala Ala Gly Ala Ser

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70	20	25	30	
72	Gln Ser Arg Arg Pro Arg Pro Pro Arg His Ala Arg Leu Gln His Leu			
73	35	40	45	
75	Pro Glu Met Thr Pro Ala Val Thr Pro Glu Gly Pro Ala Pro Pro Arg			
76	50	55	60	
78	Thr Gly Ala Trp Gln Arg Lys Asp Trp Ser Arg Ala Pro Pro Pro Pro			
79	65	70	75	80
81	Glu Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro Ser			
82	85	90	95	
84	Arg Ala Pro Pro Gln Gln Pro Gln Pro Pro Arg Met Gln Thr Gly Arg			
85	100	105	110	
87	Gly Gly Ser Ala Pro Arg Pro Glu Leu Gly Pro Pro Thr Asn Pro Phe			
88	115	120	125	
90	Gln Ala Ala Val Ala Arg Gly Leu Arg Pro Pro Leu His Asp Pro Asp			
91	130	135	140	
93	Thr Glu Ala Pro Thr Glu Ala Cys Val Thr Ser Trp Leu Trp Ser Glu			
94	145	150	155	160
96	Gly Glu Gly Ala Val Phe Tyr Arg Val Asp Leu His Phe Ile Asn Leu			
97	165	170	175	
99	Gly Thr Pro Pro Leu Asp Glu Asp Gly Arg Trp Asp Pro Ala Leu Met			
100	180	185	190	
102	Tyr Asn Pro Cys Gly Pro Glu Pro Pro Ala His Val Val Arg Ala Tyr			
103	195	200	205	
105	Asn Gln Pro Ala Gly Asp Val Arg Gly Val Trp Gly Lys Gly Glu Arg			
106	210	215	220	
108	Thr Tyr Ala Glu Gln Asp Phe Arg Val Gly Thr Arg Trp His Arg			
109	225	230	235	240
111	Leu Leu Arg Met Pro Val Arg Gly Leu Asp Gly Asp Thr Ala Pro Leu			
112	245	250	255	
114	Pro Pro His Thr Thr Glu Arg Ile Glu Thr Arg Ser Ala Arg His Pro			
115	260	265	270	
117	Trp Arg Ile Arg Phe Gly Ala Pro Gln Ala Phe Leu Ala Gly Leu Leu			
118	275	280	285	
120	Leu Ala Ala Val Ala Val Gly Thr Ala Arg Ala Gly Leu Gln Pro Arg			
121	290	295	300	
123	Ala Asp Met Ala Ala Pro Pro Met Pro Pro Gln Pro Pro Arg Ala His			
124	305	310	315	320
126	Gly Gln His Tyr Gly His His His Gln Leu Pro Phe Leu Gly His			
127	325	330	335	
129	Asp Gly His His Gly Gly Thr Leu Arg Val Gly Gln His His Arg Asn			
130	340	345	350	
132	Ala Ser Asp Val Leu Pro Gly His Trp Leu Gln Gly Gly Trp Gly Cys			
133	355	360	365	
135	Tyr Asn Leu Ser Asp Trp His Gln Gly Thr His Val Cys His Thr Lys			
136	370	375	380	
138	His Met Asp Phe Trp Cys Val Glu His Asp Arg Pro Pro Pro Ala Thr			
139	385	390	395	400
141	Pro Thr Ser Leu Thr Thr Ala Ala Asn Tyr Ile Ala Ala Ala Thr Pro			
142	405	410	415	

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144	Ala	Thr	Ala	Pro	Pro	Pro	Cys	His	Ala	Gly	Leu	Asn	Asp	Ser	Cys	Gly
145									420		425					430
147	Gly	Phe	Leu	Ser	Gly	Cys	Gly	Pro	Met	Arg	Leu	Pro	Thr	Ala	Leu	Thr
148									435		440					445
150	Pro	Gly	Ala	Val	Gly	Asp	Leu	Arg	Ala	Val	His	His	Arg	Pro	Val	Pro
151									450		455					460
153	Ala	Tyr	Pro	Val	Cys	Cys	Ala	Met	Arg	Trp	Gly	Leu	Pro	Pro	Trp	Glu
154									465		470					480
156	Leu	Val	Ile	Leu	Thr	Ala	Arg	Pro	Glu	Asp	Gly	Trp	Thr	Cys	Arg	Gly
157									485		490					495
159	Val	Pro	Ala	His	Pro	Gly	Thr	Arg	Cys	Pro	Glu	Leu	Val	Ser	Pro	Met
160									500		505					510
162	Gly	Arg	Ala	Thr	Cys	Ser	Pro	Ala	Ser	Ala	Leu	Trp	Leu	Ala	Thr	Ala
163									515		520					525
165	Asn	Ala	Leu	Ser	Leu	Asp	His	Ala	Phe	Ala	Ala	Phe	Val	Leu	Leu	Val
166									530		535					540
168	Pro	Trp	Val	Leu	Ile	Phe	Met	Val	Cys	Arg	Arg	Ala	Cys	Arg	Arg	Pro
169									545		550					560
171	Ala	Pro	Pro	Pro	Pro	Ser	Pro	Gln	Ser	Ser	Cys	Arg	Gly	Thr	Thr	Pro
172									565		570					575
174	Pro	Ala	Tyr	Gly	Glu	Glu	Ala	Phe	Thr	Tyr	Leu	Cys	Thr	Ala	Pro	Gly
175									580		585					590
177	Cys	Ala	Thr	Gln	Thr	Pro	Val	Pro	Val	Arg	Leu	Ala	Gly	Val	Gly	Phe
178									595		600					605
180	Glu	Ser	Lys	Ile	Val	Asp	Gly	Gly	Cys	Phe	Ala	Pro	Trp	Asp	Leu	Glu
181									610		615					620
183	Ala	Thr	Gly	Ala	Cys	Ile	Cys	Glu	Ile	Pro	Thr	Asp	Val	Ser	Cys	Glu
184									625		630					640
186	Gly	Leu	Gly	Ala	Trp	Val	Pro	Thr	Ala	Pro	Cys	Ala	Arg	Ile	Trp	Asn
187									645		650					655
189	Gly	Thr	Gln	Arg	Ala	Cys	Thr	Phe	Trp	Ala	Val	Asn	Ala	Tyr	Ser	Ser
190									660		665					670
192	Gly	Gly	Tyr	Ala	Gln	Leu	Ala	Ser	Tyr	Phe	Asn	Pro	Gly	Gly	Ser	Tyr
193									675		680					685
195	Tyr	Lys	Gln	Tyr	His	Pro	Thr	Ala	Cys	Glu	Val	Glu	Pro	Ala	Phe	Gly
196									690		695					700
198	His	Ser	Asp	Ala	Ala	Cys	Trp	Gly	Phe	Pro	Thr	Asp	Thr	Val	Met	Ser
199									705		710					720
201	Val	Phe	Ala	Leu	Ala	Ser	Tyr	Val	Gln	His	Pro	His	Lys	Thr	Val	Arg
202									725		730					735
204	Val	Lys	Phe	His	Thr	Glu	Thr	Arg	Thr	Val	Trp	Gln	Leu	Ser	Val	Ala
205									740		745					750
207	Gly	Val	Ser	Cys	Asn	Val	Thr	Thr	Glu	His	Pro	Phe	Cys	Asn	Thr	Pro
208									755		760					765
210	His	Gly	Gln	Leu	Glu	Val	Gln	Val	Pro	Pro	Asp	Pro	Gly	Asp	Leu	Val
211									770		775					780
213	Glu	Tyr	Ile	Met	Asn	Tyr	Thr	Gly	Asn	Gln	Gln	Ser	Arg	Trp	Gly	Leu
214									785		790					800
216	Gly	Ser	Pro	Asn	Cys	His	Gly	Pro	Asp	Trp	Ala	Ser	Pro	Val	Cys	Gln

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	805	810	815
219	Arg His Ser Pro Asp Cys Ser Arg	Leu Val Gly Ala Thr Pro	Glu Arg
220	820	825	830
222	Pro Arg Leu Arg Leu Val Asp Ala Asp Asp	Pro Leu Leu Arg Thr Ala	
223	835	840	845
225	Pro Gly Pro Gly Glu Val Trp Val Thr Pro Val	Ile Gly Ser Gln Ala	
226	850	855	860
228	Arg Lys Cys Gly Leu His Ile Arg Ala Gly Pro Tyr Gly His Ala Thr		
229	865	870	875
231	Val Glu Met Pro Glu Trp Ile His Ala His Thr Thr Ser Asp Pro Trp		
232	885	890	895
234	His Pro Pro Gly Pro Leu Gly Leu Lys Phe Lys Thr Val Arg Pro Val		
235	900	905	910
237	Ala Leu Pro Arg Ala Leu Ala Pro Pro Arg Asn Val Arg Val Thr Gly		
238	915	920	925
240	Cys Tyr Gln Cys Gly Thr Pro Ala Leu Val Glu Gly Leu Ala Pro Gly		
241	930	935	940
243	Gly Gly Asn Cys His Leu Thr Val Asn Gly Glu Asp Val Gly Ala Phe		
244	945	950	955
246	Pro Pro Gly Lys Phe Val Thr Ala Ala Leu Leu Asn Thr Pro Pro Pro		
247	965	970	975
249	Tyr Gln Val Ser Cys Gly Glu Ser Asp Arg Ala Ser Ala Gly His		
250	980	985	990

253 (2) INFORMATION FOR SEQ ID NO: 2:

255 (i) SEQUENCE CHARACTERISTICS:

- 256 (A) LENGTH: 21 amino acids
- 257 (B) TYPE: amino acid
- 258 (C) STRANDEDNESS:
- 259 (D) TOPOLOGY: unknown

265 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

267	Pro Ser Arg Ala Pro Pro Gln Gln Pro Gln Pro Pro Arg Met Gln Thr		
268	1	5	10
270	Gly Arg Gly Gly Ser		
271	20		

273 (2) INFORMATION FOR SEQ ID NO: 3:

275 (i) SEQUENCE CHARACTERISTICS:

- 276 (A) LENGTH: 7 amino acids
- 277 (B) TYPE: amino acid
- 278 (C) STRANDEDNESS:
- 279 (D) TOPOLOGY: unknown

285 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

287	Gln Pro Gln Pro Pro Arg Met		
288	1	5	

290 (2) INFORMATION FOR SEQ ID NO: 4:

292 (i) SEQUENCE CHARACTERISTICS:

- 293 (A) LENGTH: 21 amino acids
- 294 (B) TYPE: amino acid
- 295 (C) STRANDEDNESS:
- 296 (D) TOPOLOGY: unknown

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302 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
304 Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro Ser Arg
305 1 5 10 15
307 Ala Pro Pro Gln Gln
308 20
310 (2) INFORMATION FOR SEQ ID NO: 5:
312 (i) SEQUENCE CHARACTERISTICS:
313 (A) LENGTH: 7 amino acids
314 (B) TYPE: amino acid
315 (C) STRANDEDNESS:
316 (D) TOPOLOGY: unknown
322 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
324 Gln Thr Pro Ala Pro Lys Pro
325 1 5
327 (2) INFORMATION FOR SEQ ID NO: 6:
329 (i) SEQUENCE CHARACTERISTICS:
330 (A) LENGTH: 21 amino acids
331 (B) TYPE: amino acid
332 (C) STRANDEDNESS:
333 (D) TOPOLOGY: unknown
339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
341 Asp Met Ala Ala Pro Pro Met Pro Pro Gln Pro Pro Arg Ala His Gly
342 1 5 10 15
344 Gln His Tyr Gly His
345 20
347 (2) INFORMATION FOR SEQ ID NO: 7:
349 (i) SEQUENCE CHARACTERISTICS:
350 (A) LENGTH: 7 amino acids
351 (B) TYPE: amino acid
352 (C) STRANDEDNESS:
353 (D) TOPOLOGY: unknown
359 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
361 Pro Pro Gln Pro Pro Arg Ala
362 1 5
364 (2) INFORMATION FOR SEQ ID NO: 8:
366 (i) SEQUENCE CHARACTERISTICS:
367 (A) LENGTH: 1063 amino acids
368 (B) TYPE: amino acid
369 (C) STRANDEDNESS:
370 (D) TOPOLOGY: unknown
376 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
378 Met Ala Ser Thr Thr Pro Ile Thr Met Glu Asp Leu Gln Lys Ala Leu
379 1 5 10 15
381 Glu Ala Gln Ser Arg Ala Leu Arg Ala Glu Leu Ala Ala Gly Ala Ser
382 20 25 30
384 Gln Ser Arg Arg Pro Arg Pro Pro Arg Gln Arg Asp Ser Ser Thr Ser
385 35 40 45
387 Gly Asp Asp Ser Gly Arg Asp Ser Gly Gly Pro Arg Arg Arg Arg Gly
388 50 55 60

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/489,850

DATE: 08/08/2001

TIME: 16:14:05

Input Set : N:\Crf3\RULE60\09489850.txt
Output Set: N:\CRF3\08082001\I489850.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23